

Serial Number: 09/528,458

ENTERED #6 02 DD / 0330

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☒ Other: Seq 8 - corrected amino acid numbering

\*Examiner: ~~The above corrections must be communicated to the applicant in the first Office Action.~~ DO NOT send a copy of this form. 3/1/95

RAW SEQUENCE LISTING                      DATE: 06/12/2000  
 PATENT APPLICATION:    US/09/578,458        TIME: 18:08:51

Input Set : A:\Pto.amc  
 Output Set: N:\CRF3\06122000\I578458.raw

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4 <110> APPLICANT: Ballinger, Dennis G.
6     Ford, John
8     Ho, Alice
10    Lin, Hai Shan
12    Pace, Ann M.
21 <120> TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods
25 <130> FILE REFERENCE: 28110/36479
C--> 29 <140> CURRENT APPLICATION NUMBER: US/09/578,458
C--> 31 <141> CURRENT FILING DATE: 2000-05-22
34 <150> PRIOR APPLICATION NUMBER: US 09/522,964
35 <151> PRIOR FILING DATE: 2000-03-10
37 <150> PRIOR APPLICATION NUMBER: US 09/316,086
38 <151> PRIOR FILING DATE: 1999-03-20
41 <160> NUMBER OF SEQ ID NOS: 20
45 <170> SOFTWARE: PatentIn Ver. 2.0
49 <210> SEQ ID NO: 1
51 <211> LENGTH: 998
53 <212> TYPE: DNA
55 <213> ORGANISM: Homo sapiens
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61 <221> NAME/KEY: CDS
63 <222> LOCATION: (54)..(512)
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72                                     Met
74                                     1
78 tgt tcc ctc ccc atg gca aga tac tac ata att aaa tat gca gac cag      104
80 Cys Ser Leu Pro Met Ala Arg Tyr Tyr Ile Ile Lys Tyr Ala Asp Gln
82                                     5          10          15
86 aag gct cta tac aca aga gat ggc cag ctg ctg gtg gga gat cct gtt      152
88 Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val Gly Asp Pro Val
90                                     20          25          30
94 gca gac aac tgc tgt gca gag aag atc tgc aca ctt cct aac aga ggc      200
96 Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Thr Leu Pro Asn Arg Gly
98                                     35          40          45
102 ttg gac cgc acc aag gtc ccc att ttc ctg ggg atc cag gga ggg agc      248
104 Leu Asp Arg Thr Lys Val Pro Ile Phe Leu Gly Ile Gln Gly Gly Ser
106 50          55          60          65
110 cgc tgc ctg gca tgt gtg gag aca gaa gag ggg cct tcc cta cag ctg      296
112 Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro Ser Leu Gln Leu
114                                     70          75          80
118 gag gat gtg aac att gag gaa ctg tac aaa ggt ggt gaa gag gcc aca      344
120 Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly Glu Glu Ala Thr
122                                     85          90          95
126 cgc ttc acc ttc ttc cag agc agc tca ggc tcc gcc ttc agg ctt gag      392
128 Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala Phe Arg Leu Glu
130                                     100         105         110

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135 Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu Pro Gln
137 115 120 125
141 cag cca gta cag ctc acc aag gag agt gag ccc tca gcc cgt acc aag 488
143 Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser Ala Arg Thr Lys
145 130 135 140 145
149 ttt tac ttt gaa cag agc tgg tag ggagacagga aactgcgttt tagccttggtg 542
151 Phe Tyr Phe Glu Gln Ser Trp
153 150
157 ccccccacc aagctcatcc tgetcaggggt ctatggtagg cagaataatg tcccccgaaa 602
161 tatgtccaca tcctaataccc aagatctgtg catatgttac catacatgtc caaagagggtt 662
165 ttgcaaatgt gattatgtta aggatcttga aatgaggaga caatcctggg ttatccttgt 722
169 gggctcagtt taatcacaaag aaggaggcag gaagggagag tcagagagag aatggaagat 782
173 accatgcttc taattttgaa gatggagtga ggggccttga gccaacatat gcagggtgtt 842
177 ttagaaggag gaaaagccaa gggaacggat tctcctctat agtctccgga aggaacacag 902
181 ctcttgacac atggatttca gctcagtgac acccatttca gacttctgac ctccacaact 962
185 ataaaataat aaacttgtgt tattgtaaac ctctgg 998
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195 <212> TYPE: PRT
197 <213> ORGANISM: Homo sapiens
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205 1 5 10 15
209 Gln Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val Gly Asp Pro
211 20 25 30
215 Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Thr Leu Pro Asn Arg
217 35 40 45
221 Gly Leu Asp Arg Thr Lys Val Pro Ile Phe Leu Gly Ile Gln Gly Gly
223 50 55 60
227 Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro Ser Leu Gln
229 65 70 75 80
233 Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly Glu Glu Ala
235 85 90 95
239 Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala Phe Arg Leu
241 100 105 110
245 Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu Pro
247 115 120 125
251 Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser Ala Arg Thr
253 130 135 140
257 Lys Phe Tyr Phe Glu Gln Ser Trp
259 145 150
265 <210> SEQ ID NO: 3
267 <211> LENGTH: 998
269 <212> TYPE: DNA
271 <213> ORGANISM: Homo sapiens
275 <220> FEATURE:
277 <221> NAME/KEY: CDS
279 <222> LOCATION: (3)..(512)

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289 1 5 10 15
293 gca gga atg tgt tcc ctc ccc atg gca aga tac tac ata att aaa tat 95
295 Ala Gly Met Cys Ser Leu Pro Met Ala Arg Tyr Tyr Ile Ile Lys Tyr
297 20 25 30
301 gca gac cag aag gct cta tac aca aga gat ggc cag ctg ctg gtg gga 143
303 Ala Asp Gln Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val Gly
305 35 40 45
309 gat cct gtt gca gac aac tgc tgt gca gag aag atc tgc aca ctt cct 191
311 Asp Pro Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Thr Leu Pro
313 50 55 60
316 aac aga ggc ttg gac cgc acc aag gtc ccc att ttc ctg ggg atc cag 239
318 Asn Arg Gly Leu Asp Arg Thr Lys Val Pro Ile Phe Leu Gly Ile Gln
320 65 70 75
324 gga ggg agc cgc tgc ctg gca tgt gtg gag aca gaa gag ggg cct tcc 287
326 Gly Gly Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro Ser
328 80 85 90 95
332 cta cag ctg gag gat gtg aac att gag gaa ctg tac aaa ggt ggt gaa 335
334 Leu Gln Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly Glu
336 100 105 110
342 gag gcc aca cgc ttc acc ttc ttc cag agc agc tca ggc tcc gcc ttc 383
344 Glu Ala Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala Phe
346 115 120 125
350 agg ctt gag gct gct gcc tgg cct ggc tgg ttc ctg tgt ggc ccg gca 431
352 Arg Leu Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro Ala
354 130 135 140
358 gag ccc cag cag cca gta cag ctc acc aag gag agt gag ccc tca gcc 479
360 Glu Pro Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser Ala
362 145 150 155
366 cgt acc aag ttt tac ttt gaa cag agc tgg tag ggagacagga aactgcgttt 532
368 Arg Thr Lys Phe Tyr Phe Glu Gln Ser Trp
W--> 370 160 165 170
374 tagccttgtg cccccaacc aagctcatcc tgctcagggt ctatggtagg cagaataatg 592
378 tcccccgaaa tatgtccaca tcctaattccc aagatctgtg catatgttac catacatgtc 652
382 caaagagggtt ttgcaaatgt gattatgtta aggatcttga aatgaggaga caatcctggg 712
386 ttatccttgt gggctcagtt taatcacaag aaggaggcag gaaggagagag tcagagagag 772
390 aatggaagat accatgcttc taattttgaa gatggagtga ggggccttga gccaacatat 832
394 gcagggtgttt ttagaaggag gaaaagccaa gggaacggat tctcctctat agtctccgga 892
398 aggaacacag ctcttgacac atggatttca gctcagtgac acccatttca gacttctgac 952
402 ctccacaact ataaaataat aaacttggtg tattgtaaac ctctgg 998
408 <210> SEQ ID NO: 4
410 <211> LENGTH: 169
412 <212> TYPE: PRT
414 <213> ORGANISM: Homo sapiens
418 <400> SEQUENCE: 4
420 Phe Gln Glu Leu Arg Ile Cys Ser Glu Asp Gln Thr Pro Leu Ile Ala
422 1 5 10 15

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426 Gly Met Cys Ser Leu Pro Met Ala Arg Tyr Tyr Ile Ile Lys Tyr Ala
428      20      25      30
432 Asp Gln Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val Gly Asp
434      35      40      45
438 Pro Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Thr Leu Pro Asn
440      50      55      60
444 Arg Gly Leu Asp Arg Thr Lys Val Pro Ile Phe Leu Gly Ile Gln Gly
446      65      70      75      80
450 Gly Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro Ser Leu
452      85      90      95
456 Gln Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly Glu Glu
458      100      105      110
462 Ala Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala Phe Arg
464      115      120      125
468 Leu Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu
470      130      135      140
474 Pro Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser Ala Arg
476 145      150      155      160
480 Thr Lys Phe Tyr Phe Glu Gln Ser Trp
482      165
488 <210> SEQ ID NO: 5
490 <211> LENGTH: 155
492 <212> TYPE: PRT
494 <213> ORGANISM: Homo sapiens
498 <400> SEQUENCE: 5
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506 Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu His
508      20      25      30
512 Ala Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg
514      35      40      45
518 Trp Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly
520      50      55      60
524 Ser Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu Thr Leu
526      65      70      75      80
530 Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys
532      85      90      95
536 Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe Glu
538      100      105      110
542 Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Val Pro Glu Ala Asp
544      115      120      125
548 Gln Pro Val Arg Leu Thr Gln Leu Pro Glu Asn Gly Gly Trp Asn Ala
550      130      135      140
554 Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp
556 145      150      155
562 <210> SEQ ID NO: 6
564 <211> LENGTH: 178
566 <212> TYPE: PRT
568 <213> ORGANISM: Rattus rattus

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580 Ile Leu Leu Phe Arg Ser Glu Ser Ala Gly His Pro Ala Gly Lys Arg
582           20           25           30
586 Pro Cys Lys Met Gln Ala Phe Arg Ile Trp Asp Thr Asn Gln Lys Thr
588           35           40           45
592 Phe Tyr Leu Arg Asn Asn Gln Leu Ile Ala Gly Tyr Leu Gln Gly Pro
594           50           55           60
598 Asn Thr Lys Leu Glu Glu Lys Ile Asp Met Val Pro Ile Asp Phe Arg
600           65           70           75           80
604 Asn Val Phe Leu Gly Ile His Gly Gly Lys Leu Cys Leu Ser Cys Val
606           85           90           95
610 Lys Ser Gly Asp Asp Thr Lys Leu Gln Leu Glu Glu Val Asn Ile Thr
612           100          105          110
616 Asp Leu Asn Lys Asn Lys Glu Glu Asp Lys Arg Phe Thr Phe Ile Arg
618           115          120          125
622 Ser Glu Thr Gly Pro Thr Thr Ser Phe Glu Ser Leu Ala Cys Pro Gly
624           130          135          140
628 Trp Phe Leu Cys Thr Thr Leu Glu Ala Asp His Pro Val Ser Leu Thr
630           145          150          155          160
634 Asn Thr Pro Lys Glu Pro Cys Thr Val Thr Lys Phe Tyr Phe Gln Glu
636           165          170          175
640 Asp Gln
648 <210> SEQ ID NO: 7
650 <211> LENGTH: 177
652 <212> TYPE: PRT
654 <213> ORGANISM: Sus scrofa
658 <400> SEQUENCE: 7
660 Met Glu Val Ser Arg Tyr Leu Cys Ser Tyr Leu Ile Ser Phe Leu Leu
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666 Phe Leu Phe His Ser Glu Thr Ala Cys His Pro Leu Gly Lys Arg Pro
668           20           25           30
672 Cys Arg Met Gln Ala Phe Arg Ile Trp Asp Val Asn Gln Lys Thr Phe
674           35           40           45
678 Tyr Leu Arg Asn Asn Gln Leu Val Ala Gly Tyr Leu Gln Gly Pro Asn
680           50           55           60
684 Thr Lys Leu Glu Glu Lys Ile Asp Val Val Pro Val Glu Pro His Phe
686           65           70           75           80
690 Val Phe Leu Gly Ile His Gly Gly Lys Leu Cys Leu Ser Cys Val Lys
692           85           90           95
696 Ser Gly Asp Glu Met Lys Leu Gln Leu Asp Ala Val Asn Ile Thr Asp
698           100          105          110
702 Leu Arg Lys Asn Ser Glu Gln Asp Lys Arg Phe Thr Phe Ile Arg Ser
704           115          120          125
708 Asp Ser Gly Pro Thr Thr Ser Phe Glu Ser Ala Ala Cys Pro Gly Trp
710           130          135          140
714 Phe Leu Cys Thr Ala Leu Glu Ala Asp Gln Pro Val Gly Leu Thr Asn
716           145          150          155          160

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VERIFICATION SUMMARY

DATE: 06/12/2000

PATENT APPLICATION: US/09/578,458

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Output Set: N:\CRF3\06122000\I578458.raw

L:29 M:270 C: Current Application Number differs, Replaced Application Number  
L:31 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:370 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3